

TITLE: NUCLEIC ACID INTERGRATION IN EUKARYOTES

Inventor: Hooykaas et al.

Docket No.: 2183-6028US

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Fig. 1

Strain	LB' T-DNA RB' CAGGATATATTCAATTGTAAAT-CTC---CGA-GG	Chromosome, coordinate and location
WT.51	⁻⁴ 5' ATTGTATTATATATTCAATTGTAAAT-CTC---CGA-GGTA 3'	XIV, 185311 (1 bp of target site DNA deleted), int. region
<i>rad50k.1</i>	⁻⁶ 5' TGTGGGTGTGATATTCAATTGTAAAT-CTC---CGA-GG 3'	XV, 1091277, tel. region
<i>rad50k.5</i>	⁻⁷ 5' GGGGGCATCAGTATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 465986, rDNA region
<i>rad50k.6</i>	⁻²⁵ 5' GAGGTAGATGTGAGAGAGTGTGTGGGTGTGAAGTCGA 3'	XV, 1091276, tel. region
<i>mre11k.4</i>	⁻³ 5' TCTGGTAGATATATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 459692/468829, rDNA region
<i>mre11k.5</i>	⁻⁸ 5' CACATATTTCTCATTCAATTGTAAAT-CTC---CGA-GG 3'	VII/X/XIII, 536090 OR 541678/ 472487 OR 483659/196667, LTR
<i>mre11k.8</i>	⁻¹¹ 5' CGACTACTTTTATATCCAATTGTAAAT-CTC---CGA-GG 3'	XIV, 6060, subtel. region
<i>mre11k.11</i>	⁻⁷ 5' GAAGAACCCATTATTCAATTGTAAAT-CTC---CGA-GG 3'	XIV, 4866, subtel. region
<i>mre11k.14</i>	⁻⁷ 5' TGGGTGTGGGTATTCAATTGTAAAT-CTC---CGA-GG 3'	VIII, 562588, tel. region
<i>mre11k.17</i>	⁻⁹ 5' TGGGTGTGGTGTGTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 5727, subtel. region
<i>xrs2k.1</i>	⁻¹⁰ 5' TGTGTGGGTGTGGGTCAATTGTAAAT-CTC---CGA-GG 3'	IX/X, 69/52, tel. region
<i>xrs2k.17</i>	⁻¹ 5' CGTCAAGGATATATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 1071797, subtel. region

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Fig. 2

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Sc 1 -----MRSVTNAFGNSGELNMGMEFGYRKADITCEAFCELSSETMFKESSLEYKSPILLEIESDEMSQLNIRP
Hs 1 MSGWESYYKTEGDEEAEFEQPCALGAGDYKMSGHSSFLASKAMFESQSIDELT-PFDMSLQOQOSIYISKELSD
At 1 -----

Sc 75 GTAICYEYYCNDAKEGIYEPIRLNATFMKENDLLEDLSSGRISLYDFMFQQTGSEKQRLSVLTFELDTFL
Hs 80 RDLAVVEYGTESKNSVNFKNFVLOQNDNPGANKLELDQFKGQOGQKRODMMGHGSIDYSL-SEVLVVCANLF
At 1 -----

Sc 155 ECPGCKQMSNKRFLFTIDKEQEAQD-IDERARLER---LTIDLFNKNFATFFGYADKPPDN-EFYSDIOLSH
Hs 155 SLP--CPKISHARVLETNEDNPHGND--SAKASART--GAGDLRTGTFLEHLKKPGG-FDILFYDIISLE-
At 16 RKG--SLKTEDKRNFLFTNEDDEFGSMRISVNEDMTSTILOAKAQILGISLPLPSOPDIQENILFYDAIGLS-

Sc 230 TIENTGLDEFDGSPSEKPTAKYFESHLAKKEVKRIFFQCPLIIDKTNFAGVKGYYTTERKASVRYKSEHEHIR
Hs 226 -DE---DLRVHFEDSKLEL--ALRSTAKETRKRAISRKLINKD--HISVGINLROGKEPP---PKLYRFTN
At 93 -DE---LIEEMPSVGQKLED--EDQ--AVLAKRIAKRITFCG--SIEENGVALRPAIPES---ETILDSTIN

Sc 310 QEAYKRENNPITG-EDTGGKIVFYYBYGOLDINLEDSQDI MEAYTQDAFLKGGFSSSKSEYENNDKSEFIV
Hs 294 EPVKAATFENTSTGGLTPSDIKRSCHYCSRIEKEEETEFARFD--DFGLMLGFKPLV-LKKHHYLPSEIFY
At 161 LPVKVERSTCTDTG-AHQDPIQTOPYKNOIFVVEELSOVKRIS--THLLLGFKPLS-CLNDHNLPSIFY

Sc 389 PFAKYEGSIRTLAELLNIRKRIALNGKLSNPHESLYTLPSS--KADYN-----EGFYTYRPFLEIRKFPSL
Hs 370 PIESLVIGSSTLFSALLIKCEKEVAACRYTPRNIPYFVALVPQEEELQKIQVTPPGFLLLPFADDKRF---
At 236 PSEKEVIGSRAFIALHSSIOLEFAAANG--GTPPRLVALVAC--EESDGGQVDEPGITSLPFAIDIRDDEL

Sc 462 LSYDDGSEKDYDNMKVVTQIMGYFNLDCYNPSDEKNPLOXHYALHDYLL---METTFDENETPNTRKES--
Hs 447 ---PEFENIAAPGOGKMKATEELRFT--YRSDSEENPLOCHENLEAALDLMEPEQAVCLLPKVERMNE-RIG
At 313 HSK-PGVAXPRAGDQHKKASALMRELELE--SVCOFANPALORHYALCALDENEIRETRCETLPDEEMNEPAV

Sc 537 EEDDSLKLYYYIRKILES-----ESEDPIIORLNKYVKIWN-----MFYKKN-----DDNSKKEEK
Hs 520 SLDETFRELHYPPDYNPBGK-VTKREHDNEGSGSKRP-EVEYSEELKTHISKGTLGKFTVPMLEACRAYGLKSGLRQ
At 391 EALLOEKQSIVGDDPDEESGAKERSKKRKAGDADDGYIYIEL-AKT---GKLEDLTVELETYLTANNLISGRKE

Sc 593 PFDKPKFNN--
Hs 598 ELLEATKRFQD
At 466 VLENNALTLTGK

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Fig. 3A

Sc 1 MISALDSPEPQNFAPSPDFKWFCEELVVKTHEVQINGTAGGKSSFKYVEIISNVEMWRKTVGMNLYEALVLAALPYR
Hs 1 -----LTFPOL-----F
At 1 -----LTFSL-----F

Sc 81 RRTYNIKAYVLIETCSYLKLPKASATEORLKQV--QRVGGGNLS--SLVEDEAKARRAEPSSKATIDVNHLYDS
Hs 11 ERMAYGIKEVLAFLYLLNLPRDEKDALLLNR--TPTGTGAGDFIAYEVLRER-CLQKSLTIQVNDLLDS
At 57 ERGSYGIKEVLAFLYLLNLPRDEKDALLLNR--TPTGTGAGDFIAYEVLRER-CLQKSLTIQVNDLLDS

Sc 157 LGDRFASGRFKKLVKSKPFLHCEEMSEVEKFFDILNRVJGGCEKILCCHPDAQYLSVLDLNVTSKLYE
Hs 88 IASN---NSAKRKDLKKK-LICLETSSAIECKMIRIIRDLKLGSSQIFSVFHNDAALENVTDIEKVCROLAC
At 137 LASS---ENRERLVLS-LICKTN---AOEKWIRIILKDLKLGSSQIFSVFHNDAALENVTDIEKVCROLAC

Sc 237 PVRLKDDDSIKVGFAPAPOLAKNLSYEKICITLHDDFVEERDGERIQHYMNYGSIKFSRPGDYTYLGAS
Hs 164 PSVGLSD--ISITFSASPLAA-IDDEHIEKDHQSEYHETKLDGEFHQHH--GVYKFSRNGYNYTORGAS
At 210 RQPHR--QDLEVGKAVPOLAMIDNAAWVAGKDVVACKFDGRIOHFN--GDTYFSRNFDPHAYAM

Sc 317 LSGAL--OHLRFIDSKECILDGEMTDAKRRVIEPGLVKGSFAEALSFNSSNVDCHPLVYVFDLYNGTSITP
Hs 239 PEGVLPFIHNAEKADIQICILDGEMTAPNTTTEKQGGKFKIK---F---MEDSDELTCYCVEDVIMVNNKKLGE
At 286 SDLIVQ---ILVD--KCILDGEMTDTSTIRFAEFGNQIAAAE---EGLDSHKQCYSAEDVLYVGDTSITP

Sc 395 LPLQRYLNSIPLNIEIVRS-----RCYVESKPSLEVALSLGSEGVLYKYNSSYNVVSF
Hs 313 ELLKPYELSSIEPFGREIVOK-----QOHTKNVIDALNEATKREGIKKQPLSIKEDKF
At 355 QLLYEREMKKKPKLGRNEXVPEGGLNVHRPSGEPSSIVVHAALVEFFKETNREGIVLRDLESKEEEDP

Sc 459 NNNWKKKPEYEEFGNLDKIGRDSGRKDSFMLGLLVLDEEYKKHQCDSSEIVDHSQENHIONSRRVKKTIISFC
Hs 377 GEGWKKKPEYSGLMVLDLYGGYGGGS-----RGGVSHFLCAENPPPGESV---FHLLS
At 435 SGKWKKKPEYR-AGALLDILIGGYGSGR-----RGGEVQFLVLAENAEANVYPRR---FISFC

Sc 539 SANGSQEFKIDRETTGHWK-TSEVAPPASILEFG---SKIPAEWIE-PSESILEIKSRSLDNTETNMQKYATNC
Hs 438 RVGGCCKMEYVGLKLAKYWP-FHRKAPSSILCGT---EPPVAIL-PCNSLLOH---AAETPSAYRTGL
At 495 RVGGLSDLEINTVSKLPVPSNEHPKKAEPFYQVTHSKESPVWILDSPEKSITLITS---DIRTERSIVAPY

Sc 614 TLYGGYCKTRYDKWTCYTLADLYESFTVRSNPSYQAESQLG-----LIRKKRKGLISDSFHOIRKQLPSNIF
Hs 508 TLRFPRIKIRDDKEWHECTLDLLELRGKASGKLASKLYIGGDDEPQEKRRKAPKVKIGTIEHLAPNANANK
At 572 TLRFPRIKIRYDKWHECDKAFVELVNSSNGTQOKOPESESTQDNKVNKSSKGEKRVSLPSFTICTDSAIR

Sc 688 GLLFVLSEVETEDTGIRIHALLEKTIVEHGGKLYNAILKRHSIGVRLISCKTECKALIDRG--YDHPNVLL
Hs 588 IKNIFEDFCVSGTDSQPPLENRIAEFGYVQNP-----PDYCYIAGSENIIVKNILSNKEDVPAWLL
At 652 KESIFSNIIYFENVPRSHLETFRHMEVNGGFSMNN---SVTICIAAEEGITYQAAKRO--DVHFSVLL

Sc 766 CIAYKLLLEENYCFNOKMRAVAERDCLGDSENDSETKLSSKSQLSLPPMGELEIDSEVPLFLFSNR-
Hs 662 CFKTSFPWOPSMHNCPSIEFAFYDCGDSYITDILNQLKEVSGIKVSNQOTPEEASLADLEYRYSWDCS
At 725 CCSRNPLPLPYEHHDAETLOLDLDESDSYWDEGLEGLKQVLSNAKES--EDSKSIDYKELCPEKRWSC-

Sc 845 ---YAYVPRRKSEDDIIRKIKLEGGATDQOSLCNIIIPYDPFL---IDCNEHEHKKQIKASDTI-----
Hs 742 PLSFRRHTVDEYAVINNSTNEGTDAIKALERFHCKVVSCLAEGVSHVGEDHSYADFKAFTF-----
At 802 ---PLSCCVYYPYSQTESTEEALLGIMAKRLMLELACQVNNLA-ASHLLAAAEPLDETIVSSESEMEKR

Sc 913 ---PKIAPVVAPEWVHSTENCQPEEDFPVNY-----
Hs 816 ---KATFKKESVVTSID-CEQENQY-----
At 878 LLLKRIIVVSSHVLSIAE-EKLCEDVYTRPKYMEESDTEESDKSEHDTTEVASQGSQOTKEPASSKIAITSSRGR

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Fig. 3B

Sc -----
Hs -----
At 957 SNTRAVKRGSRSTNSLQRVQRRRGKQPSKISGDETEESDASEEKVSTRLS DIAETDSFGEAQRNSSRGKCAKRGKSRVG

Sc -----
Hs -----
At 1037 QTQRVQSRRGKKAAKIGGDESDENDELGNNNVSADAEENAGRSVENEETREPDIKYTESQQRDNTVAVEEALQDS

Sc -----
Hs -----
At 1117 RNAKTEMDMKEKLQIHEDPLQAMLMKMFPIPSQKTTETSNRTTGEYRKANVSCECESSEKRK LDAETDNTSVNAGAESDV

Sc -----
Hs -----
At 1197 VPPLVKKKKVSYRDVAGELLKDW

Fig. 4

Sc 1 MDYPDP-D---TIRILITTDNHIGYNENFPTGDDSRTFHEEMLAKNNHVLMAQSGLFHVNKPSZELYQVLKTLF
Hs 1 MSTADALDDENITFVLVATDILHLGMEKDAARGNDIEVILFEIERLACENEVDILLGGDLFHENKPSRKTLLHTCLETLR
At 1 MSREDFSD---TIRFLVATDCHLGYMEKDEIRRHDSFKAEIRICSAIEKQVDEILLGGDLFHENKPSPTTLVKAIEILF

Sc 77 LCCMGDKPCLELSDPSQVHHDEFTEVNYEDPNENISIPVFGISGNHDDASGDSLLCFDILHATGLNHFGRKE--
Hs 81 FYCMGDRPVQFEALSDQSVNFGSKPEWVNYDCMNLISIPVFSIHGNHDDPGACALCAIDILSCAGFVNHFGRSSES--
At 78 HCHNDKPVQFLASDQVNEQN-AGEGVNYEDFENFGVPVFSIHGNHDDPAGVCNLSAIDILSACNLVNYEGRSLLGG

Sc 155 --SEKIKVPELLEQKGSTNGALYGLFAVRDERLIRITKD-GVTTDEVTPRE---GWFNLECHQNHGHTNTAETPE
Hs 159 --VAKIDISPVLQKGSTKALYGLSIPDERLNRMEVN-KVTMRPKED---NSWFNLFVHQNRKKGSTNFIPF
At 157 SGVQQTTEYELIKKGSTTALYGLGNIRDERLNRMEQTPLEVOVLRPECEGCDVSWFNLELVHQNRVSNPKNAISF

Sc 228 QFLDFELDFVIWGHEHECPNLVKNPIKNEFLOPGSSVATSLCSEAOPKYVFELIIRYGEAPMTPIPLETPTFRMK
Hs 232 QFLDDFIDVIWGHEHECKIAPTNEQQLFYLQPGSSVVTSLSPGEAVKKHVGLLRK-GRKMMHKIPLHTVFOFFME
At 237 HFLERFELDFVWGHEHECLIDQEVSGMGFHIQPGSSVATSLIAGEKPKHVLLIIT-GNOYPTRIPLTVRPFYET

Sc 308 STSLQVPHL-RPHL---KDATSKLLEQVEENIRDANEEFOILLDDGEGDMVAEPKPLRLRVLDYSAPSNTQSPIDF
Hs 311 LIVLAHPDIFNEDPKVTATQSTCEKEEENIENA---EEELNSH---PEKPLVRLRVLDYSG-----F
At 316 LIVLKDESIL-DPNE---QSTLEHLDKVVRNLEKA---EKAENRS---EKLPLVRVLDYSG-----F

Sc 384 QVENRRFSHFVGRVANGLEFCFVRSVPVTSKKSGLNGCSDEEDVEKLFSESGGELEVTLVN---DLLNKLQI
Hs 374 EPFSVLRFQKEVDRVANPKDIHFLARQNEEG-EEINFGKLT---PSEGTLRVEDLVKQYFQTAENQDL
At 373 MTINPQRFQKIVGVANPDITIEKSKASK-GRSE-ANLDEERL---PEELNQONDEALV---AESNKE

Sc 460 SLLPEVGLNEAVKRFVDKENTAKREFSHEISNEVGILSTEEFLITDDADE--KALIKOVRANSVRPTP--PENN
Hs 447 SLITERGGEAVQEFVDRTERDTEELVKYLE-----KTEFLKIRHIAE-EDKDEEVPRFRETQKN--TNEED
At 438 ELLPVNDLDVALLNFVKDRNLAFYSCVOYNLO-----ETRGALAKSDAKKFEEDDLILKVGECLEERLDRSTPTG

Sc 536 ---FAFNGNGLDSTRSSNREVRV-SPLITQSHEDNESRITISQESSKPTKPEL---RVF---FAVKKIP
Hs 517 DE---GRESTRARALRSQEEASAFSAD-DLMSDLAEQANDSISISATNKGRRG--RCRRGGRGQNSAEGG--
At 512 SFFSTLTSENLTGSSGIANASFDDDEDTQSGGLAPPTGRRSSANTIGRPLTRGF--GRKASAMKQMT

Sc 602 -AFSDSTVIS-DAENELDNNDACQDVIDENDEIM---VSTEEEL-ASGLLNGRKTKIRPASTK---ASRGIGR
Hs 591 -QRGRFSTTROQPSRNVTAKNSEVLDDESVDIEDIFFTSKTD-QRSTSSSNIMQSQVSKGVDFEEDDDDDP
At 590 LDSLLEFQS-QRSASAAAGAAKSASTIGEDDVFS---PSSEVPEDNKPDSSEDESTKKGRRPAPRGGGR

Sc 674 NSRTP---NTFI---IGSLLAKR--K-----
Hs 669 FMNTSS-LRNRR---DIYLLALEN-MQETG-KMICYKL-----FVY-SLRF
At 666 SGTSKRGRKNSSSSLNRLLSKDDDEDEDEDEDEKKLNKSQPRVTRNYGALRR

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Fig. 5

Sc 1 -----MSAAYKKSIOGIRSFDSNDK-----TIEFGPLTLIVGMNGGKTTTIECLKYATIGDLPPN--KGVFIHDEKAT
Hs 1 MLIFSVRDMFAKMSILGRSFGIEDAKKQITFFSPLTLIVGPNAGAGKTTTIECLKYICTGDEPPG--KGNFIHDEPKVA
At 1 -----MSTEDKMLIKGIRSFDPKSN-----ETTFEPLTLIVGANGAGKTTTIECLKVSCTGLLPPNARSCHFIHDPKVA

Sc 72 GEDHRAQKLAFTFANGINAVITRNJOLMKNKTTTFFKTLEGOLVAINNS-GRSILSRSLEADATPLYLGVPKAIL
Hs 80 QETDRAQILLOFDVNGELIAVORSVCTQSKTEFKTLEGVITRT-K-GEKVLSYCAEDREKISSLGVSKAFL
At 73 GETDRAQIKLREFAAGKDA-CIRSFOLTQASMEKRAESVLOTINPHAGEKVCLSYRCALDREKIPALGVSKAIL

Sc 151 EYVIFCHOEDSLNPLSEPSNLKKKFDEIFQAMTKALINLSKTRDMSVITLLKOSFEHLKDKPKAKPLSTHGLC
Hs 158 NNVIFCHOEDSNWPLSEKALKKDFEITFSATRYIKALETLQEPOTQOKFEESQELKYLNQYKFACEIRKQITSKE
At 153 ENVIFVHQESNWNPLQFPSTLKKKFDITFSATRYTKALEVFKKLNKQDQOIKTKKLENLQTLKDAAYKERESTAGOC

Sc 231 TTEQYNEEVSEHECOLNETTESDKFEFSNOFFORILSKVENLKNITLES-DCVRLSNSIDILPLKPLNLNLANI
Hs 238 AQTSSKETVKSyenELDPKKNKNEFEENSKMKLONEKALDSRKQEKDSELEBKKEKFGQTDQOLNLYNH
At 233 ESTESSKVOLESESSSKDAENKEMMKDKRKLQDOVSITKADSSFFRIGQYAAPEENEDTIEBKWKSK

Sc 310 SVLMKRNQLRDEETSSKDRSSLSLSNSLRROCELLAGRETYEKN-FNLSLKEAFQKFOGLSNIENSDMA
Hs 318 QETMRKEREKLVCHREDEKINKESRLLEKSELLEQGLCLQANRQEHIFARDSLICSLATOLELQGFERGFSE
At 313 EERLALLGTRKEREVDTEITSSILKAKNYLSTSLCTEAFHMLLKNERDSALCNFFHYNLGNVSTEFSTE

Sc 389 QVNHEMSQKAFESDLTDITDQFAKLIQKETNLSDLKSTITVDSQNEY-NKDKSEKSHDS--EELAEKLSKSLS
Hs 398 QKKNFKLKHQEROEGEAKTACLMNDFAKETLQKQOLIEIRDRKGLR-IIELESELSKKNELNHYLQOLEG
At 393 VVLALTNRHSRAGELEMLDKKKSSETALSTAWDCYELANDRWSTIESOKRADEIRAGISRIENELERSSEFEI

Sc 466 MODSNHELENLKYTERKQSWESENTPKLNQRIEENINERITLENQIENFDRIMKTNOADLYARKGTRKSINTKL
Hs 476 SADRLELDELILKAERELSKABNSNETIKMETISLONEKADLETTERKIDOEHTCNHHTTTQOEKATDEKAD
At 473 SEVDKOTDERENQVQVLEKTRKNSERGFESKTEOKCHETYSLEKIKITLNREREVAGDAED-LITRIDECKDRIR

Sc 546 FEOKITEFLODSRIQFPLTCEORALEMDQOIFINMORNAINNKHEHLDRYTNALYNLTIEKLODNQKS
Hs 556 EOTKIKSHSD-----ETSLGYPNKKOLELSSKS--KEINQTRDLAKLNELASSEONKNHINNELERKEEQ
At 552 GVLGRLPPEKD-----MKREYCALRSIREYDLSLKS--EAEKEVNMLOMKIQEYNS--LFKHNDKTESERYI

Sc 626 KERHIOILSENPEPCTIDYNDLEETELSYTALENLKMCTTLEFNVALIAERDSCCYECSRKFE--NESFKSKL
Hs 628 LSSYEDKLFVCGSQDRESLDRKEETEKSSORAMLACATASQFITOLTENQS--CCFECORVQTEALQEAIS
At 622 ESKQALKQESSTIDAPKLLSAREKRDREYNMANGMOLEPFEKARQHS--CECCERSFT-ADBEASTIK

Sc 704 LOEYKTFDNTFKILKDTQNEKEYLHSLREKHIIINSEN-EKIDNSORCLKAKETKTSKSKLDEEVDSTME
Hs 706 DLQSKLLAPLKLKTESEKKEKRRDEELGAPRQIDLKEKEIFELRNKLONVNRQORLANDQOETLLETIM
At 697 KORRASSTELKALAVESSNASVFOOLDKRAFEEYSKLTTEIILAEHTLGEHTELGOKSEALDELGLSKOT

Sc 783 DEKELAESERELEKFTYEKELKDENSSTSEELSIYNTS-EDGCTVDELEDOORSNDLELRKTESDLOEKE
Hs 786 PEEESAKVC-TD-TIMRFOELKDEKIAQAAKLOG-IDLETTQVNOEOKOKLDESSKELNKLKIQOQ
At 777 ADKASIEALQO-LENARFOELVSYQOEDMEYKLDFRGLGVATDESELSSLSKSKLGELEKRELDQYME

Sc 863 EKVRENSRMNLKKEKLTSELESSOKONKTSRSKRENDDSRVKLEARISIKNKEEAOQVLAKYNER
Hs 864 EOIOHLKSTTNEKSEKQSTNLORROQ--DEQTVELSTE-SLYRMKAKEQSELETTLEKFOKKEINEN
At 856 RDISCLOARWHADEKAKAMLRDTK--AEEDERLAEKSOLDLVEYLTGAGPLSKEREOLLSYNEFIERN

Sc 943 IQVNNCKTADIRLRFQTIYNVDFEAGFDELQTTIKLELNL-----AQMLELKEOLELKSNEEKEKRLAD
Hs 941 TSNIAQKENDIKEKVKNHGYMKIESHIQDGDYMKQETSK-----VIAQISECEKREKENEERLMDQDOT
At 933 QEYEELAKKRYQEVVALKASYKINCFTFYDLKKGELLDQKORLSDQLOSCAANKHAGEBURNKDLRN

Sc 1018 SNTEENLKNLELIELSLOLHIESETSLVON--EERDKYQESSLRTRELSSENAGKLGKQOLNODSLT
Hs 1017 CKIOERWLODNLTLRKNEELKEEEGKOLK--OMOLOKSEHONLEENTNKRNHMLALGRONGYEEETIE
At 1013 CDILRRNEDNLNYRTTAKSEETRETESLEOPLNIECAAEASINILRREDELSSELNRCRTSVYESSISN

Sc 1097 LR-TDYKDIEKNYKEWELQTRSFVTDIDYYSKALDSAIMKHCNNINIIDELWARTYSGTDIDTIRSRDE
Hs 1096 KELREPCDAERYEMIVETTELKNDLDYYELDQAIMKHEMKNEEINKIRLWSTYRGODIYIEIRSDA
At 1093 VELQOQYKDINKHFOXTOLITTEANKOLDRYNALDKAMVTHMKNEEINKIRELWOOTYRGODIYIIS

Sc 1176 VS---SVVKGFSYNYRVVMYKQDVLEDMRGCSAGQKVLASLIIRLALFETEGANCGIALDEPTTNLDENIESLA
Hs 1176 ENVSALDRRNYNRYVMYKGDALDMRGCSAGQKVLASLIIRLALAETFCINCIGIALDEPTTNLDRENIESLA
At 1173 G-----AGTRSYSYVMOTGDTELEMRGCSAGQKVLASLIIRLALAETFCINCIGIALDEPTTNLDGPNSESAGAI

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Fig. 6

		1		50
At	(1)	-----MIGVDSKSSSTTFLETMVESEKTKHTC		
Hs	(1)	-----MERKISR		
Sc	(1)	MSQLTEFISCIPVNEEQNEEDERGLCKIQIEDGAMLETLDENSLSGTRI		
Consensus	(1)		IETL E SKIS	
		51		100
At	(28)	LRLEESGADPIFVKGTWHN---SRFDISVTDGSSS-----		
Hs	(8)	IHLVSEPSITHFLQVSWEKTLESCEVITITUGHSA-----		
Sc	(51)	EKMLYSEG TGITFSKSTFGINDLRIFTGENIDEESKKYVWYELLKMLTGHK		
Consensus	(51)	IKLLIS A IFLK SW S F ISLTDG SA		
		101		150
At	(60)	-----WICNATEEEVAERAAQWDQPVSEYL-KLAEQYLGFO		
Hs	(43)	-----WTGTVSESEISQEADDMAMEKGKYV GELRKALLSGA		
Sc	(101)	VYIASLDEKVVFTKWTICRMQDDEVWKVVMELLES---SAITRKLAELTTHPV		
Consensus	(101)		WTC MSEDEVA A DLD S YI KLAE L	
		151		200
At	(95)	QPNVVSFSDALEGSKRTISWTFEKEGTHKLEWRWKCKPSTDSKKITVGILLD		
Hs	(79)	GPADVYTFNFESKESCYFFFEKNLKDVSFRLGSFNLEKVENPAEVIRELIC		
Sc	(149)	KKGETDLFEMADKLYKDICCVDNSYRNKESDSSNRNRVQLARERELLD		
Consensus	(151)	PADVYSF A E K I NDKD S KE F K DD I RELLD		
		201		250
At	(145)	FLMEANIRLSEEVYNKTR-SFEKMRSEAERCLAQGEKLCDEKTEFESATY		
Hs	(129)	YCLDTIAENQAKNEHLOK-ENERLLRDWNDVQGRFEKCVSAKEALETDLY		
Sc	(199)	KLETRDERTRAMMVTLLNEKKKKIRELHELLRONNIKLSDDVDLSALI		
Consensus	(201)	FLLET E S MM K E EKLIRE DILAQ EK LSDKD LESALY		
		251		300
At	(194)	----AKFLSVLNA--KKAKLR-----ALRDKEDSVRVVEE-----		
Hs	(178)	----KFFILVLNE--KKTKIR-----SLHNKLLNAAQEREKDIKQEGE		
Sc	(249)	NTEVOKPISELNSPGKRMRRKTVVEPONLOKKLKDTSRRRANRKISNQS		
Consensus	(251)	KFISVLNA KK KIR AL KL A RE		
		301		350
At	(223)	-----EESTDKAESFEESGRSDDEKSEEEASKKATSSKARGGKRAARS---		
Hs	(215)	TAICSEMTADRDVPYDESTDDESENQTDLSGLASAAVSKDDSIISLDTV		
Sc	(299)	VIKMEDDDFDDFOFFGLSKRPIITAKDKLSEKYDDITSFGDDTQSISFES		
Consensus	(301)	EDS DK FD SK DD A DDL S KASAA SKGD S S S		
		351		400
At	(265)	-----		
Hs	(265)	DIAPSRKRRORMQNLGTEPKMAPOENQLOEKEKPDSSLPEITSKEHISA		
Sc	(349)	DSSSDVQKHLVSLEDNGIQISAGRSDEYGDISGSESETDASAGEKKSSN		
Consensus	(351)	D A K G A D D DS SA S		
		401		423
At	(265)	-----		
Hs	(315)	ENMSLETLRNSSPEDLFDEI---		
Sc	(399)	HSEQSGNDREPCLQTESETDIET		
Consensus	(401)	R D		